

RAW SEQUENCE LISTING

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Application Serial Number: 10/523,479
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PATENT APPLICATION: US/10/523,479 TIME: 08:43:33

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3 <110> APPLICANT: MORAN, MAGDALENE M.
4 CHONG, JAYHONG A.
5 RAMSEY, IAN SCOTT
6 CLAPHAM, DAVID E.
8 <120> TITLE OF INVENTION: SPERM-SPECIFIC CATION CHANNEL, CATSPER-3, AND
USES
9 THEREFOR
11 <130> FILE REFERENCE: 110313.138US2
13 <140> CURRENT APPLICATION NUMBER: 10/523,479
14 <141> CURRENT FILING DATE: 2005-02-04
16 <150> PRIOR APPLICATION NUMBER: PCT/US03/24432
17 <151> PRIOR FILING DATE: 2003-08-04
19 <150> PRIOR APPLICATION NUMBER: 60/401,863
20 <151> PRIOR FILING DATE: 2002-08-07
22 <160> NUMBER OF SEQ ID NOS: 7
24 <170> SOFTWARE: PatentIn Ver. 3.3
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27 <211> LENGTH: 1203
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 cgcgcctctc ccctgcagag taccattcac gagtcctacg gtccggccaga ggagcaagtg 180
35 ctcatcaacc gccagggaaat cacgaacaaa gcggacgcct gggacatgca ggagttcatc 240
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38 cactatgagt tggtctctac catagatgac attgtgctga ccattcttct ttgtgaggtt 420
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41 atcaactaca ctctcagggc gcttcgtctg gtgcattgtgt gcatggcggt ggagccctc 600
42 gcccggatca tccgcgtcat cctgcagtcg gtgcctgaca tggccaatat catggctctc 660
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44 cccaaacatt tccagaacat acagttgcg ctgtacaccc tcttcattctg catcacccag 780
45 gacggctggg tggacatcta cagtgcattc cagacagaga agagggata tgcaatggag 840
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47 ctgttgcgtca tcgtgggtac caccaacctg gagaaatgta tgaaggcagg agagcaggaa 960
48 caacagcaac gaataaccc ttgtgagaca ggcgcagagg aagaggagga gaatgaccag 1020
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50 cttgcgggag gccccctgtc gaacctctca gaaaacacgt gtgacaactt ttgcttggtg 1140
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52 tag 1203
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56 <211> LENGTH: 400

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65     20          25          30
67 Gly Ala Val Ala Ala Leu Arg Gly Arg Pro Ser Pro Leu Gln Ser Thr
68     35          40          45
70 Ile His Glu Ser Tyr Gly Arg Pro Glu Glu Gln Val Leu Ile Asn Arg
71     50          55          60
73 Gln Glu Ile Thr Asn Lys Ala Asp Ala Trp Asp Met Gln Glu Phe Ile
74     65          70          75          80
76 Thr His Met Tyr Ile Lys Gln Leu Leu Arg His Pro Ala Phe Gln Leu
77     85          90          95
79 Leu Leu Ala Leu Leu Val Ile Asn Ala Ile Thr Ile Ala Leu Arg
80     100         105         110
82 Thr Asn Ser Tyr Leu Asp Gln Lys His Tyr Glu Leu Phe Ser Thr Ile
83     115         120         125
85 Asp Asp Ile Val Leu Thr Ile Leu Leu Cys Glu Val Leu Leu Gly Trp
86     130         135         140
88 Leu Asn Gly Phe Trp Ile Phe Trp Lys Asp Gly Trp Asn Ile Leu Asn
89     145         150         155         160
91 Phe Ile Ile Val Phe Ile Leu Leu Leu Arg Phe Phe Ile Asn Glu Ile
92     165         170         175
94 Asn Ile Pro Ser Ile Asn Tyr Thr Leu Arg Ala Leu Arg Leu Val His
95     180         185         190
97 Val Cys Met Ala Val Glu Pro Leu Ala Arg Ile Ile Arg Val Ile Leu
98     195         200         205
100 Gln Ser Val Pro Asp Met Ala Asn Ile Met Val Leu Ile Leu Phe Phe
101     210         215         220
103 Met Leu Val Phe Ser Val Phe Gly Val Thr Leu Phe Gly Ala Phe Val
104     225         230         235         240
106 Pro Lys His Phe Gln Asn Ile Gln Val Ala Leu Tyr Thr Leu Phe Ile
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110     260         265         270
112 Glu Lys Arg Glu Tyr Ala Met Glu Ile Gly Gly Ala Ile Tyr Phe Thr
113     275         280         285
115 Ile Phe Ile Thr Ile Gly Ala Phe Ile Gly Ile Asn Leu Phe Val Ile
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118 Val Val Thr Thr Asn Leu Glu Gln Met Met Lys Ala Gly Glu Gln Gly
119     305         310         315         320
121 Gln Gln Gln Arg Ile Thr Phe Ser Glu Thr Gly Ala Glu Glu Glu
122     325         330         335
124 Glu Asn Asp Gln Leu Pro Leu Val His Cys Val Val Ala Arg Ser Glu
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127 Lys Ser Gly Leu Leu Gln Glu Pro Leu Ala Gly Gly Pro Leu Ser Asn
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130 Leu Ser Glu Asn Thr Cys Asp Asn Phe Cys Leu Val Leu Glu Ala Ile
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 148 agagatgtca tggagaagaa ggatgcctgg gatgtacagg aattcatcac tcaaatagttat 180
 149 atcaaggcagt tgctccgcca tccggccttc cagctgctgc tggccttct gctgtgtcc 240
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 151 ttctcgacca tagatgacat tttgttgacg atccttatct gcggaggtct gcttggttgg 360
 152 cttAACGGCT tctggatttt ctggaaaggat ggcttggaaata tcctcaactt cgcaattgtc 420
 153 ttatcttgt ttatggggtt cttcataaaa caacttgaca tggttgcccc cacctaccct 480
 154 ctcagggtgc tccggctggt gcatgtgtgt atggcggtgg aaccctggc cagaatcatc 540
 155 aaggttatcc tgcagtcgt gccagacttg gccaatgtca tggctctcat cctcttc 600
 156 atgctggat tctctgtgtt tgggttcacg ctcttcgggt catttgcgc caagcatttc 660
 157 cagaacatgg ggggtgcct gtacacgcgtc ttcatctgca tcactcgagg tggatggctg 720
 158 gacatctaca ctgacttcca gatggatgaa agagagtacg cgatggaggt cggggggcgc 780
 159 atctactttt ccgtctttat caccctcggt gccttcattt gtctcaactt gttcgctgc 840
 160 gtggtgacca caaaccttgg acaaatagtat aagaccggcg aggaagaggg acacctgaac 900
 161 ataaagttt ctgagacaga agaggatgag gactggaccg acgagctgc actggtgcat 960
 162 tgtacagagg cccgcaagga tacttccact gtcccaagg aaccacttgtt tggggggccc 1020
 163 ctgagtaacc tcacagaaaa gacctgcgt aacttctgt tggtgctga agcaatacag 1080
 164 gagaacttga tggagttacaa agagatccga gaggaactca acatgatcggt ggaggaagt 1140
 165 tcctccatcc ggttcaaccca ggagcagcaa aatgtatcc tacacaagta tacctccaaa 1200
 166 agcgccaccc tcctaagcga gccccccagaa ggggctaaaca agcaagactt gatcaactgc 1260
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 183 Glu Glu Gln Val Leu Ile Asn Arg Arg Asp Val Met Glu Lys Lys Asp
 184 35 40 45
 186 Ala Trp Asp Val Gln Glu Phe Ile Thr Gln Met Tyr Ile Lys Gln Leu
 187 50 55 60
 189 Leu Arg His Pro Ala Phe Gln Leu Leu Leu Ala Phe Leu Leu Leu Ser
 190 65 70 75 80
 192 Asn Ala Ile Thr Ile Ala Leu Arg Thr Asn Ser Tyr Leu Gly Gln Lys
 193 85 90 95

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 198 Ile Cys Glu Val Leu Leu Gly Trp Leu Asn Gly Phe Trp Ile Phe Trp
 199 115 120 125
 201 Lys Asp Gly Trp Asn Ile Leu Asn Phe Ala Ile Val Phe Ile Leu Phe
 202 130 135 140
 204 Met Gly Phe Phe Ile Lys Gln Leu Asp Met Val Ala Ile Thr Tyr Pro
 205 145 150 155 160
 207 Leu Arg Val Leu Arg Leu Val His Val Cys Met Ala Val Glu Pro Leu
 208 165 170 175
 210 Ala Arg Ile Ile Lys Val Ile Leu Gln Ser Met Pro Asp Leu Ala Asn
 211 180 185 190
 213 Val Met Ala Leu Ile Leu Phe Phe Met Leu Val Phe Ser Val Phe Gly
 214 195 200 205
 216 Val Thr Leu Phe Gly Ala Phe Val Pro Lys His Phe Gln Asn Met Gly
 217 210 215 220
 219 Val Ala Leu Tyr Thr Leu Phe Ile Cys Ile Thr Gln Asp Gly Trp Leu
 220 225 230 235 240
 222 Asp Ile Tyr Thr Asp Phe Gln Met Asp Glu Arg Glu Tyr Ala Met Glu
 223 245 250 255
 225 Val Gly Gly Ala Ile Tyr Phe Ala Val Phe Ile Thr Leu Gly Ala Phe
 226 260 265 270
 228 Ile Gly Leu Asn Leu Phe Val Val Val Val Thr Thr Asn Leu Glu Gln
 229 275 280 285
 231 Met Met Lys Thr Gly Glu Glu Gly His Leu Asn Ile Lys Phe Thr
 232 290 295 300
 234 Glu Thr Glu Glu Asp Glu Asp Trp Thr Asp Glu Leu Pro Leu Val His
 235 305 310 315 320
 237 Cys Thr Glu Ala Arg Lys Asp Thr Ser Thr Val Pro Lys Glu Pro Leu
 238 325 330 335
 240 Val Gly Gly Pro Leu Ser Asn Leu Thr Glu Lys Thr Cys Asp Asn Phe
 241 340 345 350
 243 Cys Leu Val Leu Glu Ala Ile Gln Glu Asn Leu Met Glu Tyr Lys Glu
 244 355 360 365
 246 Ile Arg Glu Glu Leu Asn Met Ile Val Glu Glu Val Ser Ser Ile Arg
 247 370 375 380
 249 Phe Asn Gln Glu Gln Gln Asn Val Ile Leu His Lys Tyr Thr Ser Lys
 250 385 390 395 400
 252 Ser Ala Thr Phe Leu Ser Glu Pro Pro Glu Gly Ala Asn Lys Gln Asp
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